

**In the Claims:**

Please cancel claims 1-28 and 49 without prejudice; amend the remaining claims as set forth below and add new claims 57-63.

1. **(Canceled)** A prokaryotic cell that is genetically modified to shift the redox status of the cytoplasm to a more oxidative state, and which further contains a gene encoding a catalyst of disulfide bond formation and/or isomerization.
2. **(Canceled)** The prokaryotic cell of claim 1, wherein the expression or activity of a reductase is decreased relative to that in the corresponding wild type cell.
3. **(Canceled)** The prokaryotic cell of claim 2, wherein the reductase is selected from the group consisting of thioredoxin reductase, glutathione reductase, and glutathione.
4. **(Canceled)** The prokaryotic cell of claim 3, in which the expression or activity of a second reductase is decreased relative to that in the corresponding wild type cell.
5. **(Canceled)** The prokaryotic cell of claim 4, wherein the second reductase is selected from the group consisting of thioredoxin reductase, glutathione reductase, and glutathione.
6. **(Canceled)** The prokaryotic cell of claim 2, wherein the gene encoding the reductase is mutated.
7. **(Canceled)** The prokaryotic cell of claim 6, wherein the gene encoding the reductase contains a null mutation.
8. **(Canceled)** The prokaryotic cell of claim 5, wherein the genes encoding the first and the second reductases contain a null mutation.
9. **(Canceled)** The prokaryotic cell of claim 2, wherein the activity of the reductase is inhibited.
10. **(Canceled)** The prokaryotic cell of claim 9, wherein the activity of the reductase is inhibited by contacting the prokaryotic cell with an agent.
11. **(Canceled)** The prokaryotic cell of claim 1, further modified to increase its ability to proliferate.
12. **(Canceled)** The prokaryotic cell of claim 4, further modified to increase its ability to proliferate.
13. **(Canceled)** The prokaryotic cell of claim 11, wherein the modification consists of the introduction of a suppressor mutation.
14. **(Canceled)** The prokaryotic cell of claim 12, wherein the modification consists of the introduction of a suppressor mutation.
15. **(Canceled)** The prokaryotic cell of claim 11, wherein the modification restores at least some of the reducing capacity to the cytoplasm of the prokaryotic cell.

16. **(Canceled)** The prokaryotic cell of claim 11, wherein the modification is a mutation in the *ahpC* gene which reduces its peroxidase activity.
17. **(Canceled)** The prokaryotic cell of claim 16, wherein the mutation is located in a region containing four triplet repeats.
18. **(Canceled)** The prokaryotic cell of claim 17, wherein the mutated *ahpC* protein has the amino acid sequence set forth in SEQ ID NO: 24.
19. **(Canceled)** The prokaryotic cell of claim 1, having ATCC Designation No. PTA-938 (FA112).
20. **(Canceled)** The prokaryotic cell of claim 1, having ATCC Designation No. PTA-939 (FA113).
21. **(Canceled)** The prokaryotic cell of claim 19, further comprising a nucleic acid encoding a catalyst of disulfide bond formation or isomerization.
22. **(Canceled)** The prokaryotic cell of claim 20, further comprising a nucleic acid encoding a catalyst of disulfide bond formation or isomerization.
23. **(Canceled)** A prokaryotic cell of claim 1, further comprising a heterologous nucleic acid.
24. **(Canceled)** The prokaryotic cell of claim 1, which comprises a nucleic acid encoding a catalyst of disulfide bond isomerization.
25. **(Canceled)** The prokaryotic cell of claim 24, which comprises a nucleic acid encoding a catalyst of disulfide bond isomerization.
26. **(Canceled)** The prokaryotic cell of claim 25, wherein the catalyst is a DsbC protein or an analog thereof which lack a signal peptide.
27. **(Canceled)** The prokaryotic cell of claim 1, wherein the catalyst is a variant of a protein of the thioredoxin superfamily having a redox potential that is higher than that of its wild type counterpart.
28. **(Canceled)** The prokaryotic cell of claim 27, wherein the variant is a "Grx" variant of thioredoxin A.
29. **(Currently amended)** A prokaryotic cell that is genetically modified to shift the redox status of the cytoplasm to a more oxidative state that favors disulfide bond formation, relative to ~~wild-type~~ a prokaryotic cell that is not genetically modified, which cell further comprises a mutated *AhpC* gene comprising an insertion of three nucleotides in the TCT triplet rich region located at about codons 36-39 of an *AhpC* gene, which insertion is further genetically modified ~~to increase~~ the cell's ability to proliferate relative to a cell that is not further genetically modified.

30. **(Previously presented)** The prokaryotic cell of claim 29, in which the expression or activity of a reductase is decreased relative to that in the corresponding wild-type cell.
31. **(Previously presented)** The prokaryotic cell of claim 30, wherein the reductase is selected from the group consisting of thioredoxin reductase and glutathione reductase.
32. **(Previously presented)** The prokaryotic cell of claim 30, in which the expression or activity of a second reductase is decreased relative to that in the corresponding wild-type cell.
33. **(Previously presented)** The prokaryotic cell of claim 29, wherein the second reductase is selected from the group consisting of thioredoxin reductase and glutathione reductase.
39. **(Currently amended)** The prokaryotic cell of claim 29, wherein the ~~further genetic modification is a suppressor mutation~~ three nucleotides are TCT.
40. **(Currently amended)** The prokaryotic cell of claim 29, wherein the ~~further modification restores at least some of the reducing capacity to the cytoplasm of the prokaryotic cell relative to cell that is not further genetically modified~~ TCT triplet rich region of the mutated *AhpC* gene encodes a stretch of four phenylalanines.
41. **(Currently amended)** The prokaryotic cell of claim 40, wherein the ~~further modification is a mutation in the *ahpC* gene which reduces its peroxidase activity~~ mutated *AhpC* gene encodes a protein comprising SEQ ID NO: 11.
42. **(Currently amended)** The prokaryotic cell of claim ~~[[41]]~~ 40, wherein the ~~mutation is located in a region containing four triplet repeats~~ TCT triplet rich region has the nucleotide sequence set forth in SEQ ID NO: 10.
43. **(Currently amended)** The prokaryotic cell of claim ~~[[42]]~~ 41, wherein the ~~mutation results in~~ mutated *AhpC* gene encodes a mutated AhpC protein that has the amino acid sequence set forth in SEQ ID NO: 24.
44. **(Original)** The prokaryotic cell of claim 29, further containing a gene encoding a catalyst of disulfide bond formation and/or isomerization.
45. **(Previously presented)** The prokaryotic cell of claim 44, wherein the catalyst is a DsbC protein which lacks a signal peptide.
46. **(Currently amended)** The prokaryotic cell of claim 44, wherein the catalyst is a variant of a protein of the thioredoxin superfamily having one or more mutation in the active site motif

CXXC (SEQ ID NO: 1) which provides the protein with a redox potential that is higher than that of its wild-type counterpart.

47. **(Original)** The prokaryotic cell of claim 46, wherein the variant is a "Grx" variant of thioredoxin A.

48. **(Original)** The prokaryotic cell of claim 44, wherein expression of the gene encoding the catalyst is inducible.

49. **(Canceled)** A method for producing a protein having at least one disulfide bond, comprising growing a host cell of claim 1 comprising a nucleic acid encoding a protein having at least one disulfide bond, under conditions in which the protein is produced, and isolating the protein from the host cell.

50. **(Currently amended)** A method for producing a protein having at least one disulfide bond comprising: growing a prokaryotic cell of claim 29 comprising a nucleic acid encoding a protein having at least one disulfide bond, under conditions in which the protein is produced, and isolating the protein from the host cell.

51-54. **(Canceled)**

55. **(Previously presented)** The prokaryotic cell of claim 29, having ATCC Accession No. PTA-938.

56. **(Previously presented)** The prokaryotic cell of claim 29, having ATCC Accession No. PTA-939.

57. **(New)** A method for producing a protein having at least one disulfide bond comprising: growing a prokaryotic cell of claim 39 comprising a nucleic acid encoding a protein having at least one disulfide bond, under conditions in which the protein is produced, and isolating the protein.

58. **(New)** A method for producing a protein having at least one disulfide bond comprising: growing a prokaryotic cell of claim 40 comprising a nucleic acid encoding a protein having at least one disulfide bond, under conditions in which the protein is produced, and isolating the protein.

59. **(New)** A method for producing a protein having at least one disulfide bond comprising: growing a prokaryotic cell of claim 41 comprising a nucleic acid encoding a protein having at

least one disulfide bond, under conditions in which the protein is produced, and isolating the protein.

60. **(New)** A method for producing a protein having at least one disulfide bond comprising: growing a prokaryotic cell of claim 42 comprising a nucleic acid encoding a protein having at least one disulfide bond, under conditions in which the protein is produced, and isolating the protein.

61. **(New)** A method for producing a protein having at least one disulfide bond comprising: growing a prokaryotic cell of claim 43 comprising a nucleic acid encoding a protein having at least one disulfide bond, under conditions in which the protein is produced, and isolating the protein.

62. **(New)** The method of claim 46, wherein the protein of the thioredoxin superfamily is TrxA.

63. **(New)** The method of claim 62, wherein the active site motif comprises SEQ ID NO: 3, 4, 5 or 6.